AMENDMENTS TO THE SPECIFICATION

PLEASE MAKE THE FOLLOWING AMENDMENTS TO THE SPECIFICATION:

Please replace the second full paragraph, lines 15-26, on page 8 of the Specification with the following paragraph:

The inventors have identified the genomic sequence corresponding to the cDNA sequence of Figure 2 (SEQ ID NO: 1), which is illustrated as bold text in Figure 3 (SEQ ID NO: 2). The coding sequence, including introns and exons, of LpTFL1 is from bases 1 to 912 of SEQ ID NO: 2. Therefore, the present invention further provides an isolated polynucleotide fragment comprising the nucleotide sequence of bases 1 to 912 (SEQ ID NO: 2) ~~or bases -78 to 1242 of Figure 3~~. Although base 1242 of SEQ ID NO: 2 corresponds to the end of the cDNA sequence, it is thought that that sequence from base 1243 to base 1624 of SEQ ID NO: 2 may comprise a polyadenylation signal. Therefore, the isolated polynucleotide fragments of the present invention may further comprise bases 1243 to 1624 of SEQ ID NO: 2 in conjunction with bases 1 to 1242 of SEQ ID NO: 2. In addition, the present invention provides a method of reducing or substantially preventing flowering in a perennial or biennial plant, the method comprising expressing a polypeptide from an isolated polynucleotide fragment comprising the nucleotide sequence of bases selected from the group consisting of bases 1 to 912, bases 1 to 1624, bases -78 to 912, bases -78 to 1242, and bases -78 to 1624, all of Figure 3 (SEQ ID NO: 2).

Please replace the last line on page 8 of the Specification with the following line:

native promoter for the LpTFL1 gene in ryegrass (bases ~~-3600 to -1~~1 to 3600 of SEQ ID NO: 2).

Please replace line 2, page 9 of the Specification with the following line:

sequence of bases -3600 to -1 of Figure 3 (bases 1 to 3600 of SEQ ID NO: 2).

Please replace line 10, page 9 of the Specification with the following line:

nucleotide sequence of bases -3600 to -1 as shown in Figure 3 (bases 1 to 3600 of SEQ ID NO: 2), or a fragment or derivative thereof

Please replace line 12, page 12 of the Specification with the following line:

YESP(K/R) located between about residues 100 and 120 of SEQ ID NO: 3~~, from the N-terminus~~.

Please replace line 20, page 16 of the Specification with the following line:

techniques based on their sequence homology to the sequence as shown in Figure 2 (SEQ ID NO: 2), or fragment,

Please replace line 6, page 19 of the Specification with the following line:

Ubiqinine promoter, and the like. In addition, the inventors have identified a 3.6kb LpTFL1 promoter (bases 1-3600 of SEQ ID NO: 2)

Please replace line 20, page 20 of the Specification with the following line:

comprising a nucleotide sequence as shown in Figure 2 (SEQ ID NO: 1), or a fragment, derivative, or homologue

Please replace line 24, page 20 of the Specification with the following line:

an isolated polypeptide having an amino acid sequence as shown in Figure 4 (SEQ ID NO: 3), or a functionally

Please replace line 11, page 21 of the Specification with the following line:

to 1624, all of Figure 3, corresponding to bases 3600 to 4512, bases 3600 to 5224, bases 3522 to 4512, bases 3522 to 4842, and bases 3522 to 5224 of SEQ ID NO: 2, respectively.

Please replace the paragraph on lines 12-21, page 21 of the Specification with the following paragraph:

In another aspect, the present invention provides an isolated polynucleotide fragment having a nucleotide sequence of bases -3600 to -1 as shown in Figure 3 (bases 1-3600 of SEQ ID NO: 2), or a fragment or derivative thereof, for up-regulating gene expression in the apex and leaves of a monocotyledonous plant during conditions that lead to flowering The present invention further provides a method of significantly reducing or substantially preventing flowering in a monocotyledonous plant, the method comprising inserting an expression cassette into a plant host cell, the expression cassette comprising a promoter and a nucleotide sequence as shown in Figure 2 (SEQ ID NO: 1), or a fragment or derivative thereof, growing the said transformed host cell in a suitable culture medium and expressing said DNA sequence to produce said protein, and wherein said expressed protein substantially reduces and/or prevents flowering in said plant.

Please replace line 26, page 21 of the Specification with the following line:

nucleotide sequence as shown in Figure 2 (SEQ ID NO: 1), or a fragment, derivative, or homologue thereof, in a

Please replace the paragraph on lines 1-5, page 22 of the Specification with the following paragraph:

In a further aspect, the present invention provides a method of significantly reducing or substantially preventing flowering in a plant, the method comprising expressing an isolated polypeptide having an amino acid sequence as shown in Figure 4 (SEQ ID NO: 3), or a functionally active fragment, derivative or homologue thereof. The isolated polypeptide is

encoded by the isolated polynucleotide fragment as shown in Figure 2 (SEQ ID NO: 1), or a fragment, derivative, or homologue thereof.

Please replace line 5, page 23 of the Specification with the following line:

to 1624, all of Figure 3, corresponding to bases 3600 to 4512, bases 3600 to 5224, bases 3522 to 4512, bases 3522 to 4842 and bases 3522 to 5224 of SEQ ID NO: 2, respectively.

Please replace line 7, page 23 of the Specification with the following line:

having a nucleotide sequence of bases -3600 to -1 as shown in Figure 3 (bases 1 to 3600 of SEQ ID NO: 2), or a fragment or

Please replace line 13 page 23 of the Specification with the following line:

Figure 2 (SEQ ID NO: 1), or a fragment or derivative thereof, growing the said transformed host cell in a suitable

Please replace line 3-6, page 25 of the Specification with the following line:

Figure 2 (SEQ ID NO: 1) illustrates the cDNA sequence of the LpTFL1 gene;

Figure 3 (SEQ ID NO: 2) illustrates the genomic sequence of the LpTFL1 gene (bases -78 to 1624) and the upstream promoter region (bases -3600 to -1), corresponding to bases 3522 to 5224 of SEQ ID NO: 2 and 1 to 3600 of SEQ ID NO: 2, respectively;

Figure 4 is the polypeptide sequence (SEQ ID NO: 3) derived from the polynucleotide sequence of Figure 2 (SEQ ID NO: 1)

Please replace lines 4-6, page 29 of the Specification with the following paragraph:

To isolate plant PEBP genes from ryegrass, a set of primers partially homologous to *TFL1* of Arabidopsis, *CEN* of *Antirrhinum,* and a rice EST (RICR2918A; accession no. 428842) were designed. Primer RY2 N (5'-GGTTATGACAGACCCAGATGTG-3') (SEQ ID NO: 15) was

used in combination with primer RY4V (5'-CGAACCTGTGGATACCAATG-3') (SEQ ID NO: 16) to amplify a 180-bp fragment by RT-PCR. Preparation of RNA for the RT-PCR used the

Please replace line 3-4, page 30 of the Specification with the following lines:

used in the reverse transcription. Two internal primers, INS5 (5'-CACATTGGTTATGACGGACC-3') (SEQ ID NO: 17) and INS3 (5'-CTCCCCCCCAAATGAAGC-3') (SEQ ID NO: 18), were used in the subsequent Real-time quantitative

Please replace line 15-16, page 30 of the Specification with the following lines:

with the primers GAP5 (5'-CAAGGACTGGAGAGGTGG-3') (SEQ ID NO: 19) and GAP3 (5'-TTGACTCGTTGTCGTACC-3') (SEQ ID NO: 20) to amplify a 380 bp *LpGAPDH* fragment. Detection of *LpTFL1* RNA

Please replace line 21-23, page 30 of the Specification with the following lines:

The coding region of *LpTFL1* cDNA was amplified using primers B0 (5'-GGATCCCCATGTCTAGGTCTGTGGAG-3') (SEQ ID NO: 21) and B550 (5'-GGGATCCCACAACTGGGATAG-CCA-3') (SEQ ID NO: 22) and recombinant *pfu* polymerase. The fragment was blunt ligated into vector pAHC27

Please replace line 2, page 32 of the Specification with the following line:

approximately 3.6kb region upstream of the transcription start (bases 1-3600 of SEQ ID NO: 2), no likely gene encoding open

Please replace lines 3-4, page 41 of the Specification with the following lines:

using primer LP0 (5'-ATGTCTAGGTCTGTGGAGCCTC-3') (SEQ ID NO: 23)in combination with primer MS8 (5'-ACCGGCAACAGGATTCAATCT-3') (SEQ ID NO: 24)to give a 560-bp fragment. Approximately 0.3 μg of genomic

Please replace line 20-21, page 41of the Specification with the following lines:

sample, a PCR was run in parallel on similar samples with the primers GAP5 (5'-CAAGGACTGGAGAGGTGG-3') (SEQ ID NO: 19) and GAP3 (5'-TTGACTCGTTGTCGTACC-3') (SEQ ID NO: 20) to amplify a 380 bp

Please replace lines 19-23, page 46 of the Specification with the following lines:

The forward primers were MS31 (5'-CGTGGCGGAGCGGCAGAC-3') (SEQ ID NO: 25), MS33 (5'-TAGTACATCCATTTAGGGTTTAGG-3') (SEQ ID NO: 26), MS56 (5'-TATTTATTTGCTTGGTACTG-3') (SEQ ID NO: 27) and LP0 (5'-ATGTCTAGGTCTGTGGAGCCTC-3') (SEQ ID NO: 23), and the reverse primers were LP4REV (5'-CGAACCTGTGGATACCAATG 3') (SEQ ID NO: 28), LP575 (5'-GGGATCCCACAACTGGGATAGCCAAGAACT-3') (SEQ ID NO: 29) and MS8 (5'-ACCGGCAACAGGATTCAATCT-3') (SEQ ID NO: 24).